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EXAMINER
KUBELIK, ANNE R

ART UNIT	PAPER NUMBER
1638	12

DATE MAILED: 12/26/2002

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No. 09/840,743	Applicant(s) FISCHER ET AL.	
	Examiner Anne R. Kubelik	Art Unit 1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *16 September 2002* .

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-29* is/are pending in the application.

4a) Of the above claim(s) *9-12, 14, 22-23 and 27-29* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-8,13,15-21 and 24-26* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12)☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

13)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____ .

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

a) ☐ The translation of the foreign language provisional application has been received.

15)☒ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449) Paper No(s) *9* .
4) ☐ Interview Summary (PTO-413) Paper No(s). _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: .

DETAILED ACTION

1. Applicant's election with traverse of Group I (claims 1-8, 13, 15-21 and 24-26) in Paper No. 11 is acknowledged. The traversal is on the ground(s) that a search of all groups would not require substantially different art searches and would thus not be burdensome. Applicant is particularly unclear why the addition of a DMT promoter in Group II justifies a new restriction group or why antisense constructs in Group III justifies a new restriction group and urges that both sense and antisense constructs result in a reduction of DMT polypeptide expression in plants.

This is not found persuasive. Group II is related to groups I and V as combination and subcombinations. Inventions in this relationship are distinct if it can be shown that (1) the combination as claimed does not require the particulars of the subcombination as claimed for patentability, and (2) that the subcombination has utility by itself or in other combinations (MPEP § 806.05(c)). In the instant case, the combination as claimed does not require the particulars of the subcombinations as claimed because different promoters can be used in the combination (see claim 10). The subcombinations have a separate utility, such as for modulating transcription using a constitutive promoter (group I, see claim 8) or for expression of heterologous nucleic acids (group V, see claims 27-29).

The methods of groups I and III are unrelated because they have different starting materials, different method steps and different end products. For example, the method of group I creates plants in which flowering is delayed, while antisense suppression results in plants with enhanced endosperm development.

The requirement is still deemed proper and is therefore made FINAL.

Claims 9-12, 14, 22-23 and 27-29 are withdrawn from consideration as being drawn to non-elected inventions.

2. In the IDS filed 4 September 2001, reference 32 was crossed out because it is not a suitable reference for publication on the face of a patent. The document has been considered.

3. The disclosure is objected to because it contains embedded hyperlinks and/or other forms of browser-executable code. See pg 17, line 23. Applicant is required to delete the embedded hyperlinks and/or other forms of browser-executable code. See MPEP § 608.01.

4. The title of the invention is not descriptive of the instant invention. A new title is required that is clearly indicative of the invention to which the claims are directed. Note that titles can be up to 500 characters long.

5. The abstract is not descriptive of the instant invention. A new abstract is required that is clearly indicative of the invention to which the claims are directed.

6. This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825.

Sequence identifiers are missing from claim 1.

Full compliance with the sequence rules is required in response to this Office action. A complete response to this Office action must include both compliance with the sequence rules and a response to the issues set forth below. Failure to fully comply with both of these requirements in the time period set forth in this Office action will be held to be non-responsive.

Claim Objections

7. Claims 5, 18 and 25 are objected to because of the following informalities:

In claim 5, part (f), "modulate" should be --modulates--.

Claim 18 has an improper article before "expression" in part (a).

Claim 25 has an improper article before "plant cell" in line 1.

Claim Rejections - 35 USC § 101

8. 35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

9. Claims 1, 4, 7-8, 13, 15-20 and 24-25 are rejected under 35 U.S.C. 101 because the claimed invention is not supported by either a specific asserted utility or a well-established utility.

Asada et al (2001, EMBL Accession No. Q94LX6) teach a nucleic acid that encodes a protein with at least 60% identity to SEQ ID NO:72. (The identity is actually higher because the program used to calculate identity counts as a mismatch a match between Xaa, where Xaa=any amino acid, and any amino acid, when in actuality it should be an exact match; these amino acids are identified with a colon on the sequence search report.) The protein taught by Asada et al is a prenyltransferase. The instant specification does not teach a specific utility for a nucleic acid that encodes a prenyltransferase.

Claim Rejections - 35 USC § 112

10. The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

11. Claims 1, 4, 7-8, 13, 15-20 and 24-25 are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a specific asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

Claims 1-2, 4-8, 13, 15-21 and 24-26 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for nucleic acids encoding SEQ ID NO:2, plants, cells and expression cassettes comprising those nucleic acids, and methods of using the expression cassettes to modify transcription of *MEDEA*, does not reasonably provide enablement for nucleic acids encoding proteins with 70% identity to SEQ ID NO:2 or with 40% identity to at least one of SEQ ID NOs:71-73, plants, cells and expression cassettes comprising those nucleic acids, and methods of using the expression cassettes to modify transcription of any gene. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.

The claims are broadly drawn to a multitude of nucleic acids encoding proteins with 70% identity to SEQ ID NO:2 or with 40% identity to at least one of SEQ ID NOs:71-73, plants, cells and expression cassettes comprising those nucleic acids, and methods of using the expression cassettes to modify transcription of any gene.

The instant specification, however, only provides guidance for characterization of *Arabidopsis dmt-1 and -2* mutants, which have fertilization-independent endosperm

development, created by T-DNA mutagenesis and use of the T-DNA to isolate the genomic clone, SEQ ID NO:1, which encodes SEQ ID NO:2 (example 1); isolation of *dmt-3*, made by another T-DNA insertion, and the conclusion that all mutant alleles are loss-of-function alleles (example 2); RNA analysis in *dmt/dmt* mutants to show that they have no *MEDEA* RNA expression (example 3), generation of transgenic plants in which DMT is overexpressed from the CaMV 35S promoter to create plants in which *MEDEA* RNA levels are increased (example 3); a BLAST search of SEQ ID NO:2 to show that DMT is a member of the HhH-GPD superfamily of DNA repair enzymes and has three domains that correspond to conserved regions of in other HhH-GPD family members (example 4); a BLAST search of databases to identify numerous related proteins and identification of consensus sequences for DMT, SEQ ID NOs:71-73 (example 4); speculation that DMT is a 5-methylcytosine glycosylase and that mutants have hypomethylation of the genome (example 5); and expression analysis of the DMT promoter, using a DMT promoter-GUS fusion gene (example 6).

The instant specification fails to provide guidance for exact hybridization or amplification conditions and probes/primers to use in isolation of nucleic acids other than SEQ ID NO:1 or 5.

The specification, on pg 18-19, suggests making conservative substitutions to produce variants proteins. However, making "conservative" substitutions does not produce predictable results. Lazar et al (1988, Mol. Cell. Biol. 8:1247-1252) showed that the "conservative" substitution of glutamic acid for aspartic acid at position 47 reduced biological function of transforming growth factor alpha while "nonconservative" substitutions with alanine or asparagine had no effect (abstract). Similarly, Hill et al (1998, Biochem. Biophys. Res. Comm. 244:573-577) teach that when three histidines that are maintained in ADP-glucose pyrophosphorylase across

several species are substituted with the "nonconservative" amino acid glutamine, there is little effect on enzyme activity, while the substitution of one of those histidines with the "conservative" amino acid arginine drastically reduced enzyme activity (see Table 1).

Given the claim breath, unpredictability, and lack of guidance as discussed above, undue experimentation would have been required by one skilled in the art to develop and evaluate nucleic acids encoding proteins with 70% identity to SEQ ID NO:2. Making all possible single amino acid substitutions in an 1729 amino acid long protein like that encoded by SEQ ID NO:1 or 5 would require making and analyzing 19^{1729} nucleic acids; these proteins would have 99.9% identity to SEQ ID NO:2. Because nucleic acids encoding proteins with 70% identity to SEQ ID NO:2 would encode proteins with 518 amino acid substitutions, many more than 19^{1729} nucleic acids would need to be made and analyzed.

As discussed above, Asada et al (2001, EMBL Accession No. Q94LX6) teach a nucleic acid that encodes a protein with at least 60% identity to SEQ ID NO:72; this protein is a prenyltransferase. The instant specification does not teach how to use a nucleic acid that encodes a prenyltransferase.

The specification states that SEQ ID NO:2 is related to endonuclease III, based on homology to a protein from *Deinococcus radiodurans* (pg 14, lines 18-20, and pg 40, lines 22-29, and pg 42, lines 4-24). However, this homology spans 191 of SEQ ID NO:2's 1729 amino acids and is only 31.4% similar. The *D. radiodurans* protein was identified in a genomic sequencing project as an endonuclease III by its having 53.3% identity to a protein from *Methanobacterium thermautotrophium* that was identified in a genomic sequencing project as an endonuclease III by its having 35% identity to a putative endonuclease III identified in a

Methanococcus jannaschii genomic sequencing project (see GenBank Accession Nos. AE002073, AE000855 and Q58030). This was not followed back further, but the point is clear. Identification of the protein of SEQ ID NO:2 as an endonuclease III or a related protein solely by homology to a series of putative endonuclease III proteins, and without other supporting data, like enzymatic activity studies, is speculative at best. Duggleby (1997, Gene 190:245-249) teach that "the function of any DNA sequence, whose identity is based solely on homology, can only be proven by experiments designed to evaluate that function" (pg 248, left column, paragraph 4). Additionally, an endonuclease III gene from *Arabidopsis* has been cloned (Roldán-Arjona et al, 2000, Plant Mol. Biol. 44:43-52). That protein has a very different sequence and is much shorter than the protein of SEQ ID NO:2.

The specification speculates, based on putative presence of a protein motif, that the protein encoded by the instant nucleic acid is an endonuclease III or a glycosylase (pg 42, lines 4-24), particularly a 5 -methylcytosine glycosylase (pg 44, lines 1-24). This conclusion is partly drawn because a mutation in an unrelated gene results in a reduction in genomic cytosine methylation and also results in phenotypic abnormalities in floral phenotype (pg 12-23). The specification also found weak homology between SEQ ID NO:2 and a series of protein fragments in the sequence databases and used those sequences to derive three consensus sequences, DMT Domains A, B and C (pg 42, line 24, to pg 43, line 28). However, the instant specification provides no evidence that SEQ ID NO:2 or any of these other proteins have the putative enzymatic function.

The specification teaches no assay to determine if any of the proteins encoded by nucleic acids encoding proteins with 70% identity to SEQ ID NO:2 or with 40% identity to at least one

of SEQ ID NOs:71-73 have this activity. Thus, nucleic acids encoding proteins with 70% identity to SEQ ID NO:2 or with 40% identity to at least one of SEQ ID NOs:71-73 are not enabled, and cells and plants transformed with those nucleic acids and methods of using those nucleic acids are also not enabled.

As the specification does not describe the transformation of any plant with any nucleic acid encoding a protein that has 70% identity to SEQ ID NO:2 or 40% identity to any of SEQ ID NO:71-73, undue trial and error experimentation would be required to screen through the myriad of nucleic acids encompassed by the claims and plants transformed therewith, to identify those with a delaying in flowering time, a modulation of chromosomal DNA methylation, or expression of the *MEDEA* gene, if such plants are even obtainable.

Given the claim breath, unpredictability in the art, undue experimentation, and lack of guidance in the specification as discussed above, the instant invention is not enabled throughout the full scope of the claims.

12. Claims 1-2, 4-8, 13, 15-21 and 24-26 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are broadly drawn to a multitude of nucleic acids that encode proteins with 70% identity to SEQ ID NO:2 or with 40% identity to at least one of SEQ ID NOs:71-73, plants, cells and expression cassettes comprising those nucleic acids, and methods of using the expression cassettes to modify transcription. In contrast, the only nucleic acid described in the specification is one that encodes SEQ ID NO:2. Applicant does not describe other DNA

molecules encompassed by the claims, and the structural features that distinguish all such nucleic acids from other nucleic acids are not provided.

Additionally, claim 1 does not describe the function of the protein encoded by the claimed nucleic acid.

Hence, Applicant has not, in fact, described nucleic acids that encode proteins with 70% identity to SEQ ID NO:2 or with 40% identity to at least one of SEQ ID NOs:71-73 within the full scope of the claims, and the specification fails to provide an adequate written description of the claimed invention.

Therefore, given the lack of written description in the specification with regard to the structural and physical characteristics of the claimed compositions, it is not clear that Applicant was in possession of the genus claimed at the time this application was filed.

See *Univ. of California v. Eli Lilly*, 119 F.3d 1559, 43 USPQ 2d 1398 (Fed. Cir. 1997):

> The name cDNA is not in itself a written description of that DNA; it conveys no distinguishing information concerning its identity. While the example provides a process for obtaining human insulin-encoding cDNA, there is no further information in the patent pertaining to that cDNA's relevant structural or physical characteristics; in other words, it thus does not describe human insulin cDNA .... Accordingly, the specification does not provide a written description of the invention ....

and at pg 1406:

> a generic statement such as "vertebrate insulin cDNA" or "mammalian insulin cDNA," without more, is not an adequate written description of the genus because it does not distinguish the genus from others, except by function. It does not specifically define any of the genes that fall within its definition. It does not define any structural features commonly possessed by members of the genus that distinguish them from others. One skilled in the art therefore cannot, as one can do with a fully described genus, visualize or recognize the identity of the members of the genus. A definition by function, as we have previously indicted, does not suffice to define the genus because it is only an indication of what the genes does, not what it is.

See *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ 2d 1016 at page 1021:

> A gene is a chemical compound, albeit a complex one, and ... conception of a chemical compound requires that the inventor be able to define it so as to distinguish it from other materials .... Conception does not occur unless one has a mental picture of the structure of the chemical or is able to define it by its method of preparation, its physical or chemical properties, or whatever characteristics sufficiently distinguish it. It is not sufficient to define it solely by it principal biological property, *e.g.*, encoding

> human erythropoietin, because an alleged conception having no more specificity than that is simply a wish to know the identity of any material with that biological property.

13. The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

14. Claims 4-8, 13, 15-21 and 24-26 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter that Applicant regards as the invention. Dependent claims are included in all rejections.

Claim 4 is indefinite in its recitation of "amino acid sequence identical to a domain of claim 1" as claim 1 is drawn to a nucleic acid, not a domain.

In claim 5, parts (a)- (j) should start with the same part of speech.

Claim 5 (f) is indefinite in its recitation of "modulate meristem stem and/or activity". It is unclear what this means. A word or words appear to be missing.

Claim 7 lacks antecedent basis for the limitation "the polynucleotide".

In claim 13, it is not clear to what the polynucleotide sequence is heterologous.

Claims 13, 15 and 24 lack antecedent basis for the limitation "polypeptide of claim 1" as claim 1 is drawn to a nucleic acid.

Claim 18 is indefinite in its recitation of "modulating transcription." First, the term "modulating" is a relative term that renders the claim indefinite. The term "modulating" is not defined by the claim, the specification does not provide a standard for ascertaining the requisite degree, and one of ordinary skill in the art would not be reasonably apprised of the metes and bounds of the invention. It is unclear if transcription is being increased, decreased, or both relative to that of a non-transgenic plant. Second, it is unclear which gene it is whose

transcription is being modulated; thus the criteria for selecting a host cell with modulated transcription is unclear.

In claim 18, part (a) a word or words appear to be missing between "cell" and "an".

Claim Rejections - 35 USC § 102

15. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

16. Because SEQ ID NOs:71-73 were not disclosed in parent application 09/553,690, the filing date of the instant application, 23 April 2001, was used as the filing date for nucleic acids encoding proteins with 40% identity to SEQ ID NOs:71, 72 or 73. The filing date for nucleic acids encoding SEQ ID NO:2 is the filing date of the parent application, 21 April 2000.

17. Claims 1 and 5-6 are rejected under 35 U.S.C. 102(b) as being anticipated by Bevan et al (1 June 1998, GenBank Accession No. O49498; 23 April 1999, GenBank Accession No. T05430; and 20 April 2000, Accession No. T48453).

Bevan et al teach a nucleic acid that encodes a protein that has 61% identity to SEQ ID NO:72 (Accession No. T48453), one encodes a protein that has 70% identity to SEQ ID NO:71 (Accession Nos. T05430), and one encodes a protein with 70% identity to SEQ ID NO:71 (Accession No. O49498). The identities are actually higher because the program used to calculate identity counts a match between Xaa, where Xaa=any amino acid, and any amino acid

as a mismatch, when in actuality it should be an exact match; these amino acids are identified with a colon on the sequence search reports. The proteins encoded by these nucleic acids would be capable of exhibiting at least one of the properties listed in claim 5 and would comprise one of the regions listed in claim 6 as all comprise at least one basic amino acid and thus have a "basic region."

18. Claims 1 and 5-6 are rejected under 35 U.S.C. 102(a) as being anticipated by Lin et al (1 May 2000, Sptrembl Accession Nos. Q9SR66 and Q9SJQ6).

Lin et al teach a nucleic acid that encodes a protein with 59% identity to SEQ ID NO:72 and 69% identity to SEQ ID NO:71 (Q9SR66) and one that encodes a protein with 69% identity to SEQ ID NO:71 (Q9SJQ6). The proteins encoded by these nucleic acids would be capable of exhibiting at least one of the properties listed in claim 5 and would comprise one of the regions listed in claim 6 as all comprise at least one basic amino acid and thus have a "basic region."

19. Claims 1-2, 4-7 and 15-16 are rejected under 35 U.S.C. 102(a) as being anticipated by Bevan et al (20 April 2000, Accession Nos. T48452, T48453, and 48454).

Bevan et al teach a nucleic acid that encodes a protein that is 99.9% identical to SEQ ID NO:2 (see sequence search results). The protein would contain an amino acid sequence identical to a domain of claim 1, would be capable of exhibiting at least one of the properties listed in claim 5, would contain at least one of the regions listed in claim 6. The nucleic acid is part of a BAC clone and as such would comprise the genomic sequence and would operably linked to a promoter. This BAC clone would be in a host cell for purposes of molecular biological manipulation.

20. Claims 1-7 and 15-16 are rejected under 35 U.S.C. 102(b) as being anticipated by Rounsley et al (1997, GenBank Accession Nos. B60854 and B28303).

Rounsley et al teach a nucleic acid that is about 99% identical to SEQ ID NO:5, which encodes SEQ ID NO:2 (see sequence search results). The protein would contain an amino acid sequence identical to a domain of claim 1, would be capable of exhibiting at least one of the properties listed in claim 5, would contain at least one of the regions listed in claim 6. The nucleic acid is part of a BAC clone and as such would comprise the native promoter. This BAC clone would be in a host cell for purposes of molecular biological manipulation.

Double Patenting

21. The nonstatutory double patenting rejection is based on a judicially created doctrine grounded in public policy (a policy reflected in the statute) so as to prevent the unjustified or improper timewise extension of the "right to exclude" granted by a patent and to prevent possible harassment by multiple assignees. An obviousness-type double patenting rejection is appropriate where the conflicting claims are not identical, but an examined application claim not is patentably distinct from the reference claim(s) because the examined claim is either anticipated by, or would have been obvious over, the reference claim(s). See *In re Goodman*, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); *In re Longi*, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985); *In re Van Ornum*, 686 F.2d 937, 214 USPQ 761 (CCPA 1982); *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970);and, *In re Thorington*, 418 F.2d 528, 163 USPQ 644 (CCPA 1969).

A timely filed terminal disclaimer in compliance with 37 CFR 1.321(c) may be used to overcome an actual or provisional rejection based on a nonstatutory double patenting ground provided the conflicting application or patent is shown to be commonly owned with this application. See 37 CFR 1.130(b).

Effective January 1, 1994, a registered attorney or agent of record may sign a terminal disclaimer. A terminal disclaimer signed by the assignee must fully comply with 37 CFR 3.73(b).

22. Claims 1-8, 13, 15-21 and 24-26 are rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims 1-38 of U.S. Patent No. 6,476,296. Although the conflicting claims are not identical, they are not patentably distinct

from each other because claims drawn to nucleic acids encoding proteins with 80% identity to SEQ ID NO:2, expression cassettes, cells and plants transformed with those nucleic acids, and methods of using the expression cassettes to modulate transcription, as claimed in the issued patent, are a species of the genus of nucleic acids encoding proteins with 70% identity to SEQ ID NO:2 or with 40% identity to at least one of SEQ ID NOs:71-73, plants, cells and expression cassettes comprising those nucleic acids, and methods of using the expression cassettes to modify transcription, as claimed in the instant application.

23. Claims 8, 13, 17-21 and 24-26 are free of the prior art, given the failure of the prior art to teach or suggest constructs comprising the nucleic acid of claim 1 operably linked to a constitutive or heterologous promoter, plants and plant cells transformed with the nucleic acid of claim 1 and methods of using the nucleic acid to modulate transcription in plants or plant cells.

Conclusion

24. No claim is allowed.

25. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Anne R. Kubelik, whose telephone number is (703) 308-5059. The examiner can normally be reached Monday through Friday, 8:30 am - 5:00 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Amy Nelson, can be reached at (703) 306-3218. The fax phone numbers for the organization where this application or proceeding is assigned are (703) 872-9306 for regular communications and (703) 872-9307 for After Final communications.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to Customer Service at (703) 308-0198.

Anne R. Kubelik, Ph.D.
December 19, 2002

DAVID T. FOX
PRIMARY EXAMINER
GROUP ~~180~~ 1638